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PCT09

RAW SEQUENCE LISTING   DATE: 08/30/2001
PATENT APPLICATION: US/09/830,144   TIME: 06:24:59

Input Set : A:\06501-076001.txt
Output Set: N:\CRF3\08292001\I830144.raw

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 4 <110> APPLICANT: Tsuchiya, Masayuki
 5         Ohtomo, Toshihiko
 6         Sugamata, Yasuhiro
 7         Matsumoto, Kunihiro
 9 <120> TITLE OF INVENTION: Method for screening compounds inhibiting signal
10        transduction through inflammatory cytokines
12 <130> FILE REFERENCE: 06501-076001
14 <140> CURRENT APPLICATION NUMBER: 09/830,144
15 <141> CURRENT FILING DATE: 2001-04-20
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05817
18 <151> PRIOR FILING DATE: 1999-10-21
20 <150> PRIOR APPLICATION NUMBER: JP 10/299962
21 <151> PRIOR FILING DATE: 1998-10-21
23 <160> NUMBER OF SEQ ID NOS: 10
25 <170> SOFTWARE: PatentIn version 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2656
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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36 <400> SEQUENCE: 1
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41 gggtctcacc cggattgtcc gggtggcacc gttcccggcc ccaccgggcg ccgcgaggga  180
43 tc atg tct aca gcc tct gcc gcc tcc tcc tcc tcc tcg tct tcg gcc     227
44    Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ser Ala
45    1               5                  10                  15
47 ggt gag atg atc gaa gcc cct tcc cag gtc ctc aac ttt gaa gag atc   275
48 Gly Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile
49                  20                  25                  30
51 gac tac aag gag atc gag gtg gaa gag gtt gtt gga aga gga gcc ttt   323
52 Asp Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe
53                  35                  40                  45
55 gga gtt gtt tgc aaa gct aag tgg aga gca aaa gat gtt gct att aaa   371
56 Gly Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys
57             50                  55                  60
59 caa ata gaa agt gaa tct gag agg aaa gcg ttt att gta gag ctt cgg   419
60 Gln Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg
61        65                  70                  75
63 cag tta tcc cgt gtg aac cat cct aat att gta aag ctt tat gga gcc   467
64 Gln Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala
65   80                  85                  90                  95
67 tgc ttg aat cca gtg tgt ctt gtg atg gaa tat gct gaa ggg ggc tct  515
68 Cys Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser
69                 100                 105                 110
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71  tta tat aat gtg ctg cat ggt gct gaa cca ttg cca tat tat act gct    563
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73              115             120             125
75  gcc cac gca atg agt tgg tgt tta cag tgt tcc caa gga gtg gct tat    611
76  Ala His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr
77              130             135             140
79  ctt cac agc atg caa ccc aaa gcg cta att cac agg gac ctg aaa cca    659
80  Leu His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro
81      145             150             155
83  cca aac tta ctg ctg gtt gca ggg ggg aca gtt cta aaa att tgt gat    707
84  Pro Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp
85  160             165             170             175
87  ttt ggt aca gcc tgt gac att cag aca cac atg acc aat aac aag ggg    755
88  Phe Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly
89              180             185             190
91  agt gct gct tgg atg gca cct gaa gtt ttt gaa ggt agt aat tac agt    803
92  Ser Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser
93              195             200             205
95  gaa aaa tgt gac gtc ttc agc tgg ggt att att ctt tgg gaa gtg ata    851
96  Glu Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile
97              210             215             220
99  acg cgt cgg aaa ccc ttt gat gag att ggt ggc cca gct ttc cga atc    899
100 Thr Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile
101     225             230             235
103 atg tgg gct gtt cat aat ggt act cga cca cca ctg ata aaa aat tta    947
104 Met Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu
105 240             245             250             255
107 cct aag ccc att gag agc ctg atg act cgt tgt tgg tct aaa gat cct    995
108 Pro Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro
109             260             265             270
111 tcc cag cgc cct tca atg gag gaa att gtg aaa ata atg act cac ttg    1043
112 Ser Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu
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115 atg cgg tac ttt cca gga gca gat gag cca tta cag tat cct tgt cag    1091
116 Met Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln
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119 tat tca gat gaa gga cag agc aac tct gcc acc agt aca ggc tca ttc    1139
120 Tyr Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe
121     305             310             315
123 atg gac att gct tct aca aat acg agt aac aaa agt gac act aat atg    1187
124 Met Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met
125 320             325             330             335
127 gag caa gtt cct gcc aca aat gat act att aag cgc tta gaa tca aaa    1235
128 Glu Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys
129             340             345             350
131 ttg ttg aaa aat cag gca aag caa cag agt gaa tct gga cgt tta agc    1283
132 Leu Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser
133             355             360             365
135 ttg gga gcc tcc cat ggg agc agt gtg gag agc ttg ccc cca acc tct    1331
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136 Leu Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser
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139 gag ggc aag agg atg agt gct gac atg tct gaa ata gaa gct agg atc      1379
140 Glu Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile
141         385             390             395
143 gcc gca acc aca ggc aac gga cag cca aga cgt aga tcc atc caa gac      1427
144 Ala Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp
145 400             405             410             415
147 ttg act gta act gga aca gaa cct ggt cag gtg agc agt agg tca tcc      1475
148 Leu Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser
149             420             425             430
151 agt ccc agt gtc aga atg att act acc tca gga cca acc tca gaa aag      1523
152 Ser Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys
153         435             440             445
155 cca act cga agt cat cca tgg acc cct gat gat tcc aca gat acc aat      1571
156 Pro Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn
157         450             455              460
159 gga tca gat aac tcc atc cca atg gct tat ctt aca ctg gat cac caa      1619
160 Gly Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln
161     465             470             475
163 cta cag cct cta gca ccg tgc cca aac tcc aaa gaa tct atg gca gtg      1667
164 Leu Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val
165 480             485             490             495
167 ttt gaa cag cat tgt aaa atg gca caa gaa tat atg aaa gtt caa aca      1715
168 Phe Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr
169             500             505             510
171 gaa att gca ttg tta tta cag aga aag caa gaa cta gtt gca gaa ctg      1763
172 Glu Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu
173             515             520             525
175 gac cag gat gaa aag gac cag caa aat aca tct cgc ctg gta cag gaa      1811
176 Asp Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu
177         530             535             540
179 cat aaa aag ctt tta gat gaa aac aaa agc ctt tct act tac tac cag      1859
180 His Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln
181     545             550             555
183 caa tgc aaa aaa caa cta gag gtc atc aga agt cag cag cag aaa cga      1907
184 Gln Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Gln Lys Arg
185 560             565             570             575
187 caa ggc act tca tgattctctg ggaccgttac attttgaaat atgcaaagaa          1959
188 Gln Gly Thr Ser
191 agactttttt tttaaggaaa ggaaaacctt ataatgacga ttcatgagtg ttagcttttt  2019
193 ggcgtgttct gaatgccaac tgcctatatt tgctgcattt ttttcattgt ttattttcct  2079
195 tttctcatgg tggacataca attttactgt ttcattgcat aacatggtag catctgtgac  2139
197 ttgaatgagc agcactttgc aacttcaaaa cagatgcagt gaactgtggc tgtatatgca  2199
199 tgctcattgt gtgaaggcta gcctaacaga acaggaggta tcaaactagc tgctatgtgc  2259
201 aaacagcgtc cattttttca tattagaggt ggaacctcaa gaatgacttt attcttgtat  2319
203 ctcatctcaa aatattaata attttttttcc caaaagatgg tatataccaa gttaaagaca  2379
205 gggtattata aatttagagt gattggtggt atattacgga aatacggaac ctttagggat  2439
207 agttccgtgt aagggctttg atgccagcat ccttggatca gtactgaact cagttccatc  2499
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228 Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe Gly
229   35   40   45
231 Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys Gln
232   50   55   60
234 Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln
235 65   70   75   80
237 Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys
238   85   90   95
240 Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu
241   100   105   110
243 Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala Ala
244   115   120   125
246 His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu
247   130   135   140
249 His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro
250 145   150   155   160
252 Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe
253   165   170   175
255 Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser
256   180   185   190
258 Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu
259   195   200   205
261 Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr
262   210   215   220
264 Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met
265 225   230   235   240
267 Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro
268   245   250   255
270 Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser
271   260   265   270
273 Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met
274   275   280   285
276 Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Tyr
277   290   295   300
279 Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe Met
280 305   310   315   320
282 Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met Glu

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283                  325                 330                 335
285 Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys Leu
286              340                 345                 350
288 Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser Leu
289          355                 360                 365
291 Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser Glu
292      370                 375                 380
294 Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile Ala
295 385                 390                 395                 400
297 Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp Leu
298              405                 410                 415
300 Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser Ser
301          420                 425                 430
303 Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys Pro
304          435                 440                 445
306 Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn Gly
307      450                 455                 460
309 Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln Leu
310 465                 470                 475                 480
312 Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val Phe
313              485                 490                 495
315 Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr Glu
316          500                 505                 510
318 Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu Asp
319      515                 520                 525
321 Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu His
322      530                 535                 540
324 Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln Gln
325 545                 550                 555                 560
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348 ctg cag agt gag cag cag cca agc tgg aca gat gac ctg cct ctc tgc   101
349 Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
350     10                  15                  20
352 cac ctc tct ggg gtt ggc tca gcc tcc aac cgc agc tac tct gct gat   149
353 His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
354 25                  30                  35                  40
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VERIFICATION SUMMARY   DATE: 08/30/2001
PATENT APPLICATION: US/09/830,144   TIME: 06:25:00

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